

SEQUENCE LISTING

<110> Olmsted, Robert  
Keith, Paula  
Dryga, Sergey  
Caley, Ian  
Maughan, Maureen  
Johnston, Robert  
Davis, Nancy  
Swanstrom, Ronald

<120> ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE AS VACCINES

<130> 01113.0001U3

<150> 09/902,537  
<151> 2001-07-09

<150> 60/216,995  
<151> 2000-07-07

<160> 19

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D  
O  
D  
E  
R  
S  
B  
D  
C  
O  
T  
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synthetic construct

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---

gct ttg cag cgg agc ttc ccg cag ttt gag gta gaa gcc aag cag gtc 96  
Ala Leu Gln Arg Ser Phe Pro Gln Phe Glu Val Glu Ala Lys Gln Val  
20 25 30

act gat aat gac cat gct aat gcc aga gcg ttt tcg cat ctg gct tca 144  
Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser  
35 40 45  
aaa ctg atc gaa acg gag gtg gac cca tcc gac acg atc ctt gac att 192  
Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile  
50 55 60

gga agt gcg ccc gcc cgc aga atg tat tct aag cac aag tat cat tgt 240  
Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys His Lys Tyr His Cys  
65 70 75 80

atc tgt ccg atg aga tgt gcg gaa gat ccg gac aga ttg tat aag tat 288  
Ile Cys Pro Met Arg Cys Ala Glu Asp Pro Asp Arg Leu Tyr Lys Tyr  
85 90 95

gca act aag ctg aag aaa aac tgt aag gaa ata act gat aag gaa ttg Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu 100 105 110	336
gac aag aaa atg aag gag ctc gcc gcc gtc atg agc gac cct gac ctg Asp Lys Lys Met Lys Glu Leu Ala Ala Val Met Ser Asp Pro Asp Leu 115 120 125	384
gaa act gag act atg tgc ctc cac gac gac gag tcg tgt cgc tac gaa Glu Thr Glu Thr Met Cys'Leu His Asp Asp Glu Ser Cys Arg Tyr Glu 130 135 140	432
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gct acg atg cac cgc gag gga ttc ttg tgc tgc aaa gtg aca gac aca Ala Thr Met His Arg Glu Gly Phe Leu Cys Cys Lys Val Thr Asp Thr 305 310 315 320	960

tta aac ggg gag agg gtc tct ttt ccc gtg tgc acg tat gtg cca gct Leu Asn Gly Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro Ala 325	330	335	1008	
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aag cgc ccg gat acc caa acc atc atc aaa gtg aac agc gat ttc cac Lys Arg Pro Asp Thr Gln Thr Ile Ile Lys Val Asn Ser Asp Phe His 435	440	445	1344	
tca ttc gtg ctg ccc agg ata ggc agt aac aca ttg gag atc ggg ctg Ser Phe Val Leu Pro Arg Ile Gly Ser Asn Thr Leu Glu Ile Gly Leu 450	455	460	1392	
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ctc att acc gcc gag gac gta caa gaa gct aag tgc gca gcc gat gag Leu Ile Thr Ala Glu Asp Val Gln Glu Ala Lys Cys Ala Ala Asp Glu 485	490	495	1488	
gct aag gag gtg cgt gaa gcc gag gag ttg cgc gca gct cta cca cct Ala Lys Glu Val Arg Glu Ala Glu Glu Leu Arg Ala Ala Leu Pro Pro 500	505	510	1536	
ttg gca gct gat gtt gag gag ccc act ctg gaa gcc gat gtc gac ttg Leu Ala Ala Asp Val Glu Glu Pro Thr Leu Glu Ala Asp Val Asp Leu 515	520	525	1584	
atg tta caa gag gct ggg gcc ggc tca gtg gag aca cct cgt ggc ttg Met Leu Gln Glu Ala Gly Ala Gly Ser Val Glu Thr Pro Arg Gly Leu 530	535	540	1632	

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cac cct ctc gct gaa caa gtc ata gtg ata aca cac tct ggc cga aaa His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys 580 585 590	1776
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acc att gtg tac aac gaa cgt gag ttc gta aac agg tac ctg cac cat Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His 625 630 635 640	1920
att gcc aca cat gga gga gcg ctg aac act gat gaa gaa tat tac aaa Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys 645 650 655	1968
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tat att gac gaa gct ttt gct tgt cat gca ggt act ctc aga gcg ctc Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu 785 790 795 800	2400
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tgg gtg aag cag ttg caa ata gat tac aaa ggc aac gaa ata atg acg Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr 900 905 910	2736
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aac gtc cta ctg acc cgc acg gag gac cgc atc gtg tgg aaa aca cta Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu 945 950 955 960	2880
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ttc act gcc acg ata gag gag tgg caa gca gag cat gat gcc atc atg Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met 980 985 990	2976

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gaa ccc aca ata cga tcg gca gtg cct tca gcg atc cag aac acg ctc Glu Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu 2065 2070 2075	6240
cag aac gtc ctg gca gct gcc aca aaa aga aat tgc aat gtc acg caa Gln Asn Val Leu Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln 2080 2085 2090 2095	6288
atg aga gaa ttg ccc gta ttg gat tcg gcg gcc ttt aat gtg gaa tgc Met Arg Glu Leu Pro Val Leu Asp Ser Ala Ala Phe Asn Val Glu Cys 2100 2105 2110	6336
ttc aag aaa tat gcg tgt aat aat gaa tat tgg gaa acg ttt aaa gaa Phe Lys Lys Tyr Ala Cys Asn Asn Glu Tyr Trp Glu Thr Phe Lys Glu 2115 2120 2125	6384

aac ccc atc agg ctt act gaa gaa aac gtg gta aat tac att acc aaa Asn Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys 2130 2135 2140	6432
tta aaa gga cca aaa gct gct ctt ttt gcg aag aca cat aat ttg Leu Lys Gly Pro Lys Ala Ala Leu Phe Ala Lys Thr His Asn Leu 2145 2150 2155	6480
aat atg ttg cag gac ata cca atg gac agg ttt gta atg gac tta aag Asn Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys 2160 2165 2170 2175	6528
aga gac gtg aaa gtg act cca gga aca aaa cat act gaa gaa cgg ccc Arg Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro 2180 2185 2190	6576
aag gta cag gtg atc cag gct gcc gat ccg cta gca aca gcg tat ctg Lys Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu 2195 2200 2205	6624
tgc gga atc cac cga gag ctg gtt agg aga tta aat gcg gtc ctg ctt Cys Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu 2210 2215 2220	6672
ccg aac att cat aca ctg ttt gat atg tcg gct gaa gac ttt gac gct Pro Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala 2225 2230 2235	6720
att ata gcc gag cac ttc cag cct ggg gat tgt gtt ctg gaa act gac Ile Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp 2240 2245 2250 2255	6768
atc gcg tcg ttt gat aaa agt gag gac gac gcc atg gct ctg acc gcg Ile Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala 2260 2265 2270	6816
tta atg att ctg gaa gac tta ggt gtg gac gca gag ctg ttg acg ctg Leu Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu 2275 2280 2285	6864
att gag gcg gct ttc ggc gaa att tca tca ata cat ttg ccc act aaa Ile Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys 2290 2295 2300	6912
act aaa ttt aaa ttc gga gcc atg atg aaa tct gga atg ttc ctc aca Thr Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr 2305 2310 2315	6960
ctg ttt gtg aac aca gtc att aac att gta atc gca agc aga gtg ttg Leu Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu 2320 2325 2330 2335	7008
aga gaa cgg cta acc gga tca cca tgt gca gca ttc att gga gat gac Arg Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp 2340 2345 2350	7056
aat atc gtg aaa gga gtc aaa tcg gac aaa tta atg gca gac agg tgc Asn Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys 2355 2360 2365	7104

gcc acc tgg ttg aat atg gaa gtc aag att ata gat gct gtg gtg ggc      7152  
 Ala Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly  
 2370                    2375                    2380

gag aaa gcg ccc tat ttc tgt gga ggg ttt att ttg tgt gac tcc gtg      7200  
 Glu Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val  
 2385                    2390                    2395

acc ggc aca gcg tgc cgt gtg gca gac ccc cta aaa agg ctg ttt aag      7248  
 Thr Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys  
 2400                    2405                    2410                    2415

ctt ggc aaa cct ctg gca gca gac gat gaa cat gat gat gac agg aga      7296  
 Leu Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg  
 2420                    2425                    2430

agg gca ttg cat gaa gag tca aca cgc tgg aac cga gtg ggt att ctt      7344  
 Arg Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu  
 2435                    2440                    2445

tca gag ctg tgc aag gca gta gaa tca agg tat gaa acc gta gga act      7392  
 Ser Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr  
 2450                    2455                    2460

tcc atc ata gtt atg gcc atg act act cta gct agc agt gtt aaa tca      7440  
 Ser Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser  
 2465                    2470                    2475

ttc agc tac ctg aga ggg gcc cct ata act ctc tac ggc      7479  
 Phe Ser Tyr Leu Arg Gly Ala Pro Ile Thr Leu Tyr Gly  
 2480                    2485                    2490

<210> 3  
<211> 2492  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 3  
Met Glu Lys Val His Val Asp Ile Glu Glu Asp Ser Pro Phe Leu Arg  
1                        5                        10                        15  
Ala Leu Gln Arg Ser Phe Pro Gln Phe Glu Val Glu Ala Lys Gln Val  
20                        25                        30  
Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser  
35                        40                        45  
Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile  
50                        55                        60  
Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys His Lys Tyr His Cys  
65                        70                        75                        80  
Ile Cys Pro Met Arg Cys Ala Glu Asp Pro Asp Arg Leu Tyr Lys Tyr  
85                        90                        95  
Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu  
100                      105                        110

Asp Lys Lys Met Lys Glu Leu Ala Ala Val Met Ser Asp Pro Asp Leu  
 115 120 125  
 Glu Thr Glu Thr Met Cys Leu His Asp Asp Glu Ser Cys Arg Tyr Glu  
 130 135 140

Gly Gln Val Ala Val Tyr Gln Asp Val Tyr Ala Val Asp Gly Pro Thr  
 145 150 155 160  
 Ser Leu Tyr His Gln Ala Asn Lys Gly Val Arg Val Ala Tyr Trp Ile  
 165 170 175  
 Gly Phe Asp Thr Thr Pro Phe Met Phe Lys Asn Leu Ala Gly Ala Tyr  
 180 185 190  
 Pro Ser Tyr Ser Thr Asn Trp Ala Asp Glu Thr Val Leu Thr Ala Arg  
 195 200 205  
 Asn Ile Gly Leu Cys Ser Ser Asp Val Met Glu Arg Ser Arg Arg Gly  
 210 215 220  
 Met Ser Ile Leu Arg Lys Lys Tyr Leu Lys Pro Ser Asn Asn Val Leu  
 225 230 235 240  
 Phe Ser Val Gly Ser Thr Ile Tyr His Glu Lys Arg Asp Leu Leu Arg  
 245 250 255  
 Ser Trp His Leu Pro Ser Val Phe His Leu Arg Gly Lys Gln Asn Tyr  
 260 265 270  
 Thr Cys Arg Cys Glu Thr Ile Val Ser Cys Asp Gly Tyr Val Val Lys  
 275 280 285  
 Arg Ile Ala Ile Ser Pro Gly Leu Tyr Gly Lys Pro Ser Gly Tyr Ala  
 290 295 300  
 Ala Thr Met His Arg Glu Gly Phe Leu Cys Cys Lys Val Thr Asp Thr  
 305 310 315 320  
 Leu Asn Gly Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro Ala  
 325 330 335  
 Thr Leu Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Ser Ala  
 340 345 350  
 Asp Asp Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val  
 355 360 365  
 Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu Leu  
 370 375 380  
 Pro Val Val Ala Gln Ala Phe Ala Arg Trp Ala Lys Glu Tyr Lys Glu  
 385 390 395 400  
 Asp Gln Glu Asp Glu Arg Pro Leu Gly Leu Arg Asp Arg Gln Leu Val  
 405 410 415

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Met-Gly-Cys-Cys-Trp-Ala-Phe-Arg-Arg-His-Lys-Ile-Thr-Ser-Ile-Tyr  
 420 425 430  
 Lys Arg Pro Asp Thr Gln Thr Ile Ile Lys Val Asn Ser Asp Phe His  
 435 440 445  
 Ser Phe Val Leu Pro Arg Ile Gly Ser Asn Thr Leu Glu Ile Gly Leu  
 450 455 460  
 Arg Thr Arg Ile Arg Lys Met Leu Glu Glu His Lys Glu Pro Ser Pro  
 465 470 475 480  
 Leu Ile Thr Ala Glu Asp Val Gln Glu Ala Lys Cys Ala Ala Asp Glu  
 485 490 495  
 Ala Lys Glu Val Arg Glu Ala Glu Glu Leu Arg Ala Ala Leu Pro Pro  
 500 505 510  
 Leu Ala Ala Asp Val Glu Glu Pro Thr Leu Glu Ala Asp Val Asp Leu  
 515 520 525  
 Met Leu Gln Glu Ala Gly Ala Gly Ser Val Glu Thr Pro Arg Gly Leu  
 530 535 540  
 Ile Lys Val Thr Ser Tyr Ala Gly Glu Asp Lys Ile Gly Ser Tyr Ala  
 545 550 555 560

Val Leu Ser Pro Gln Ala Val Leu Lys Ser Glu Lys Leu Ser Cys Ile  
 565 570 575  
 His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys  
 580 585 590  
 Gly Arg Tyr Ala Val Glu Pro Tyr His Gly Lys Val Val Val Pro Glu  
 595 600 605  
 Gly His Ala Ile Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala  
 610 615 620  
 Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His  
 625 630 635 640  
 Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys  
 645 650 655  
 Thr Val Lys Pro Ser Glu His Asp Gly Glu Tyr Leu Tyr Asp Ile Asp  
 660 665 670  
 Arg Lys Gln Cys Val Lys Lys Glu Leu Val Thr Gly Leu Gly Leu Thr  
 675 680 685  
 Gly Glu Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu  
 690 695 700  
 Arg Thr Arg Pro Ala Ala Pro Tyr Gln Val Pro Thr Ile Gly Val Tyr  
 705 710 715 720  
 Gly Val Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr  
 725 730 735  
 Lys Lys Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile  
 740 745 750  
 Ile Arg Asp Val Lys Lys Met Lys Gly Leu Asp Val Asn Ala Arg Thr  
 755 760 765  
 Val Asp Ser Val Leu Leu Asn Gly Cys Lys His Pro Val Glu Thr Leu  
 770 775 780  
 Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu  
 785 790 795 800  
 Ile Ala Ile Ile Arg Pro Lys Lys Ala Val Leu Cys Gly Asp Pro Lys  
 805 810 815  
 Gln Cys Gly Phe Phe Asn Met Met Cys Leu Lys Val His Phe Asn His  
 820 825 830

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Glu Ile Cys Thr Gln Val Phe His Lys Ser Ile Ser Arg Arg Cys Thr  
 835 840 845  
 Lys Ser Val Thr Ser Val Val Ser Thr Leu Phe Tyr Asp Lys Lys Met  
 850 855 860  
 Arg Thr Thr Asn Pro Lys Glu Thr Lys Ile Val Ile Asp Thr Thr Gly  
 865 870 875 880  
 Ser Thr Lys Pro Lys Gln Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly  
 885 890 895  
 Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr  
 900 905 910  
 Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg  
 915 920 925  
 Tyr Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Thr Ser Glu His Val  
 930 935 940  
 Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu  
 945 950 955 960  
 Ala Gly Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asn  
 965 970 975  
 Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met  
 980 985 990

Arg His Ile Leu Glu Arg Pro Asp Pro Thr Asp Val Phe Gln Asn Lys  
 995 1000 1005  
 Ala Asn Val Cys Trp Ala Lys Ala Leu Val Pro Val Leu Lys Thr Ala  
 1010 1015 1020  
 Gly Ile Asp Met Thr Thr Glu Gln Trp Asn Thr Val Asp Tyr Phe Glu  
 1025 1030 1035 1040  
 Thr Asp Lys Ala His Ser Ala Glu Ile Val Leu Asn Gln Leu Cys Val  
 1045 1050 1055  
 Arg Phe Phe Gly Leu Asp Leu Asp Ser Gly Leu Phe Ser Ala Pro Thr  
 1060 1065 1070  
 Val Pro Leu Ser Ile Arg Asn Asn His Trp Asp Asn Ser Pro Ser Pro  
 1075 1080 1085  
 Asn Met Tyr Gly Leu Asn Lys Glu Val Val Arg Gln Leu Ser Arg Arg  
 1090 1095 1100  
 Tyr Pro Gln Leu Pro Arg Ala Val Ala Thr Gly Arg Val Tyr Asp Met  
 1105 1110 1115 1120  
 Asn Thr Gly Thr Leu Arg Asn Tyr Asp Pro Arg Ile Asn Leu Val Pro  
 1125 1130 1135  
 Val Asn Arg Arg Leu Pro His Ala Leu Val Leu His His Asn Glu His  
 1140 1145 1150  
 Pro Gln Ser Asp Phe Ser Ser Phe Val Ser Lys Leu Lys Gly Arg Thr  
 1155 1160 1165  
 Val Leu Val Val Gly Glu Lys Leu Ser Val Pro Gly Lys Met Val Asp  
 1170 1175 1180  
 Trp Leu Ser Asp Arg Pro Glu Ala Thr Phe Arg Ala Arg Leu Asp Leu  
 1185 1190 1195 1200  
 Gly Ile Pro Gly Asp Val Pro Lys Tyr Asp Ile Ile Phe Val Asn Val  
 1205 1210 1215  
 Arg Thr Pro Tyr Lys Tyr His His Tyr Gln Gln Cys Glu Asp His Ala  
 1220 1225 1230  
 Ile Lys Leu Ser Met Leu Thr Lys Lys Ala Cys Leu His Leu Asn Pro  
 1235 1240 1245  
 Gly Gly Thr Cys Val Ser Ile Gly Tyr Gly Tyr Ala Asp Arg Ala Ser  
 1250 1255 1260

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Glu Ser Ile Ile Gly Ala Ile Ala Arg Gln Phe Lys Phe Ser Arg Val  
 1265 1270 1275 1280  
 Cys Lys Pro Lys Ser Ser Leu Glu Glu Thr Glu Val Leu Phe Val Phe  
 1285 1290 1295

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Ile Gly Tyr Asp Arg Lys Ala Arg Thr His Asn Pro Tyr Lys Leu Ser  
 1300 1305 1310  
 Ser Thr Leu Thr Asn Ile Tyr Thr Gly Ser Arg Leu His Glu Ala Gly  
 1315 1320 1325  
 Cys Ala Pro Ser Tyr His Val Val Arg Gly Asp Ile Ala Thr Ala Thr  
 1330 1335 1340  
 Glu Gly Val Ile Ile Asn Ala Ala Asn Ser Lys Gly Gln Pro Gly Gly  
 1345 1350 1355 1360  
 Gly Val Cys Gly Ala Leu Tyr Lys Lys Phe Pro Glu Ser Phe Asp Leu  
 1365 1370 1375  
 Gln Pro Ile Glu Val Gly Lys Ala Arg Leu Val Lys Gly Ala Ala Lys  
 1380 1385 1390  
 His Ile Ile His Ala Val Gly Pro Asn Phe Asn Lys Val Ser Glu Val  
 1395 1400 1405

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Glu Gly Asp Lys Gln Leu Ala Glu Ala Tyr Glu Ser Ile Ala Lys Ile  
 1410 1415 1420

Val Asn Asp Asn Asn Tyr Lys Ser Val Ala Ile Pro Leu Leu Ser Thr  
 1425 1430 1435 1440  
 Gly Ile Phe Ser Gly Asn Lys Asp Arg Leu Thr Gln Ser Leu Asn His  
 1445 1450 1455  
 Leu Leu Thr Ala Leu Asp Thr Thr Asp Ala Asp Val Ala Ile Tyr Cys  
 1460 1465 1470  
 Arg Asp Lys Lys Trp Glu Met Thr Leu Lys Glu Ala Val Ala Arg Arg  
 1475 1480 1485  
 Glu Ala Val Glu Glu Ile Cys Ile Ser Asp Asp Ser Ser Val Thr Glu  
 1490 1495 1500  
 Pro Asp Ala Glu Leu Val Arg Val His Pro Lys Ser Ser Leu Ala Gly  
 1505 1510 1515 1520  
 Arg Lys Gly Tyr Ser Thr Ser Asp Gly Lys Thr Phe Ser Tyr Leu Glu  
 1525 1530 1535  
 Gly Thr Lys Phe His Gln Ala Ala Lys Asp Ile Ala Glu Ile Asn Ala  
 1540 1545 1550  
 Met Trp Pro Val Ala Thr Glu Ala Asn Glu Gln Val Cys Met Tyr Ile  
 1555 1560 1565  
 Leu Gly Glu Ser Met Ser Ser Ile Arg Ser Lys Cys Pro Val Glu Glu  
 1570 1575 1580  
 Ser Glu Ala Ser Thr Pro Pro Ser Thr Leu Pro Cys Leu Cys Ile His  
 1585 1590 1595 1600  
 Ala Met Thr Pro Glu Arg Val Gln Arg Leu Lys Ala Ser Arg Pro Glu  
 1605 1610 1615  
 Gln Ile Thr Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr Arg Ile Thr  
 1620 1625 1630  
 Gly Val Gln Lys Ile Gln Cys Ser Gln Pro Ile Leu Phe Ser Pro Lys  
 1635 1640 1645  
 Val Pro Ala Tyr Ile His Pro Arg Lys Tyr Leu Val Glu Thr Pro Pro  
 1650 1655 1660  
 Val Asp Glu Thr Pro Glu Pro Ser Ala Glu Asn Gln Ser Thr Glu Gly  
 1665 1670 1675 1680  
 Thr Pro Glu Gln Pro Pro Leu Ile Thr Glu Asp Glu Thr Arg Thr Arg  
 1685 1690 1695

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Thr Pro Glu Pro Ile Ile Glu Glu Glu Glu Asp Ser Ile Ser  
 1700 1705 1710  
 Leu Leu Ser Asp Gly Pro Thr His Gln Val Leu Gln Val Glu Ala Asp  
 1715 1720 1725  
 Ile-His-Gly-Pro-Pro-Ser-Val-Ser-Ser-Ser-Ser-Trp-Ser-Ile-Pro-His  
 1730 1735 1740  
 Ala Ser Asp Phe Asp Val Asp Ser Leu Ser Ile Leu Asp Thr Leu Glu  
 1745 1750 1755 1760  
 Gly Ala Ser Val Thr Ser Gly Ala Thr Ser Ala Glu Thr Asn Ser Tyr  
 1765 1770 1775  
 Phe Ala Lys Ser Met Glu Phe Leu Ala Arg Pro Val Pro Ala Pro Arg  
 1780 1785 1790  
 Thr Val Phe Arg Asn Pro Pro His Pro Ala Pro Arg Thr Arg Thr Pro  
 1795 1800 1805  
 Ser Leu Ala Pro Ser Arg Ala Cys Ser Arg Thr Ser Leu Val Ser Thr  
 1810 1815 1820

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Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Leu Glu Ala Leu  
 1825 1830 1835 1840  
 Thr Pro Ser Arg Thr Pro Ser Arg Ser Val Ser Arg Thr Ser Leu Val  
 1845 1850 1855

Ser Asn Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Phe Glu  
                  1860                 1865                 1870  
 Ala Phe Val Ala Gln Gln Gln Arg Phe Asp Ala Gly Ala Tyr Ile Phe  
                  1875                 1880                 1885  
 Ser Ser Asp Thr Gly Gln Gly His Leu Gln Gln Lys Ser Val Arg Gln  
                  1890                 1895                 1900  
 Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile Ser  
                  1905                 1910                 1915                 1920  
 Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys Lys  
                  1925                 1930                 1935  
 Leu Gln Leu Asn Pro Thr Pro Ala Asn Arg Ser Arg Tyr Gln Ser Arg  
                  1940                 1945                 1950  
 Lys Val Glu Asn Met Lys Ala Ile Thr Ala Arg Arg Ile Leu Gln Gly  
                  1955                 1960                 1965  
 Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg Thr  
                  1970                 1975                 1980  
 Leu His Pro Val Pro Leu Tyr Ser Ser Val Asn Arg Ala Phe Ser  
                  1985                 1990                 1995                 2000  
 Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu Asn  
                  2005                 2010                 2015  
 Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala Tyr  
                  2020                 2025                 2030  
 Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser Phe  
                  2035                 2040                 2045  
 Cys Pro Ala Lys Leu Arg Ser Phe Pro Lys Lys His Ser Tyr Leu Glu  
                  2050                 2055                 2060  
 Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu Gln  
                  2065                 2070                 2075                 2080  
 Asn Val Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln Met  
                  2085                 2090                 2095  
 Arg Glu Leu Pro Val Leu Asp Ser Ala Ala Phe Asn Val Glu Cys Phe  
                  2100                 2105                 2110  
 Lys Lys Tyr Ala Cys Asn Asn Glu Tyr Trp Glu Thr Phe Lys Glu Asn  
                  2115                 2120                 2125

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Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys Leu  
                  2130                 2135                 2140  
 Lys Gly Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu Asn  
                  2145                 2150                 2155                 2160  
 Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys Arg  
                  2165                 2170                 2175  
 Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro Lys  
                  2180                 2185                 2190  
 Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu Cys  
                  2195                 2200                 2205  
 Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu Pro  
                  2210                 2215                 2220  
 Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala Ile  
                  2225                 2230                 2235                 2240

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Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp Ile  
                  2245                 2250                 2255  
 Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala Leu  
                  2260                 2265                 2270  
 Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu Ile  
                  2275                 2280                 2285

Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys Thr  
 2290 2295 2300  
 Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr Leu  
 2305 2310 2315 2320  
 Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu Arg  
 2325 2330 2335  
 Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp Asn  
 2340 2345 2350  
 Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys Ala  
 2355 2360 2365  
 Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly Glu  
 2370 2375 2380  
 Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val Thr  
 2385 2390 2395 2400  
 Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys Leu  
 2405 2410 2415  
 Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg Arg  
 2420 2425 2430  
 Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu Ser  
 2435 2440 2445  
 Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr Ser  
 2450 2455 2460  
 Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser Phe  
 2465 2470 2475 2480  
 Ser Tyr Leu Arg Gly Ala Pro Ile Thr Leu Tyr Gly  
 2485 2490

<210> 4  
 <211> 1476  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct  
  
 <221> CDS  
 <222> (1)...(1476)

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<400>-4  
 atg gct gcg aga gcg tca ata tta aga ggg gaa aaa tta gat aaa tgg 48  
 Met Ala Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp  
 1 5 10 15  
  
 gaa aag att agg tta agg cca ggg gga aag aaa cat tat atg tta aaa 96  
 Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys  
 20 25 30  
  
 cac ata gta tgg gcg agc agg gag ctg gaa aga ttt gca ctt aac cct 144  
 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro  
 35 40 45  
  
 ggc ctt tta gaa aca tca gaa gga tgt aaa caa ata atg aaa cag cta 192  
 Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys Gln Leu  
 50 55 60

caa cca gct ctc cag aca gga aca gag gaa ctt aaa tca tta tac aac Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu Tyr Asn 65 70 75 80	240
aca gta gca act ctc tat tgt gta cat gaa aag ata gaa gta cga gac Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp 85 90 95	288
acc aag gaa gcc tta gat aag ata gag gaa gaa caa aac aaa tgt cag Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln 100 105 110	336
caa aaa acg cag cag gca aaa gcg gct gac ggg aaa gtc agt caa aat Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser Gln Asn 115 120 125	384
tat cct ata gtg cag aat ctc caa ggg caa atg gta cat caa gcc ata Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile 130 135 140	432
tca cct aga acc ttg aat gca tgg gta aaa gta ata gaa gaa aag gct Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala 145 150 155 160	480
ttt agc cca gag gta ata ccc atg ttt aca gca tta tca gaa gga gcc Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala 165 170 175	528
acc cca caa gat tta aac acc atg tta aat aca gtg ggg gga cac caa Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln 180 185 190	576
gca gcc atg caa atg tta aaa gat act att aat gaa gag gct gca gaa Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu 195 200 205	624
tgg gat aga tta cat cca gtc cat gcg ggg cct att gca cca ggc cag Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln 210 215 220	672
atg aga gaa cca agg gga agt gac ata gca gga act act agt acc ctt Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu 225 230 235 240	720
cag gaa caa ata gca tgg atg aca agt aac cca cct att cca gtg gga Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly 245 250 255	768
gac atc tat aaa aga tgg ata att ctg ggg tta aat aaa ata gtg aga Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg 260 265 270	816
atg tat agc ccg gtc agc att ttg gac ata aga caa ggg cca aag gaa Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu 275 280 285	864

ccc ttt cga gac tat gta gat cggttc ttt aaa act tta aga gct gaa Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu 290 295 300	912
caa gct aca caa gaa gta aaa aat tgg atg aca gac acc ttg tta gtc Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val 305 310 315 320	960
caa aat gcg aac cca gat tgt aag acc att ttg aga gca tta gga cca Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro 325 330 335	1008
ggg gct aca tta gaa gaa atg atg aca gca tgt caa ggg gtg gga gga Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly 340 345 350	1056
cct ggc cac aaa gca aga gta ttg gct gag gca atg agt caa aca aac Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn 355 360 365	1104
agt gga aac ata atg atg cag aga agc aat ttt aaa ggc cct aga aga Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro Arg Arg 370 375 380	1152
att gtt aaa tgt ttt aac tgt ggc aag gaa ggg cac ata gcc aga aat Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn 385 390 395 400	1200
tgc aga gcc cct agg aaa aaa ggc tgt tgg aaa tgt gga aaa gaa gga Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly 405 410 415	1248
cac caa atg aaa gac tgc act gag agg cag gct aat ttt tta ggg aaa His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys 420 425 430	1296
att tgg cct tcc cac aag ggg agg cca ggg aat ttc ctt cag aac aga Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg 435 440 445	1344
cca gag cca aca gcc cca gca gag agc ttc agg ttc gaa gag aca Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr 450 455 460	1392
acc ccc gct ccg aaa cag gag ccg ata gaa agg gaa ccc tta act tcc Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser 465 470 475 480	1440
ctc aaa tca ctc ttt ggc agc gac ccc ttg tct caa Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln 485 490	1476

<210> 5  
<211> 492  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 5

Met	Ala	Ala	Arg	Ala	Ser	Ile	Leu	Arg	Gly	Glu	Lys	Leu	Asp	Lys	Trp
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Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	His	Tyr	Met	Leu	Lys
						20				25					30
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Leu	Asn	Pro
						35				40					45
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Lys	Gln	Ile	Met	Lys	Gln	Leu
						50				55					60
Gln	Pro	Ala	Leu	Gln	Thr	Gly	Thr	Glu	Glu	Leu	Lys	Ser	Leu	Tyr	Asn
						65				70					80
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Glu	Lys	Ile	Glu	Val	Arg	Asp
						85				90					95
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Cys	Gln
						100				105					110
Gln	Lys	Thr	Gln	Gln	Ala	Lys	Ala	Ala	Asp	Gly	Lys	Val	Ser	Gln	Asn
						115				120					125
Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile
						130				135					140
Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Ile	Glu	Glu	Lys	Ala
						145				150					160
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Thr	Ala	Leu	Ser	Glu	Gly	Ala
						165				170					175
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln
						180				185					190
Ala	Ala	Met	Gln	Met	Leu	Lys	Asp	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu
						195				200					205
Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln
						210				215					220
Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu
						225				230					240
Gln	Glu	Gln	Ile	Ala	Trp	Met	Thr	Ser	Asn	Pro	Pro	Ile	Pro	Val	Gly
						245				250					255
Asp	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	.Arg
						260				265					270
Met	Tyr	Ser	Pro	Val	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu
						275				280					285
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Phe	Lys	Thr	Leu	Arg	Ala	Glu
						290				295					300
Gln	Ala	Thr	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Asp	Thr	Leu	Leu	Val
						305				310					320
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Arg	Ala	Leu	Gly	Pro
						325				330					335
Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly
						340				345					350
Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	Gln	Thr	Asn
						355				360					365
Ser	Gly	Asn	Ile	Met	Met	Gln	Arg	Ser	Asn	Phe	Lys	Gly	Pro	Arg	Arg
						370				375					380
Ile	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His	Ile	Ala	Arg	Asn
						385				390					400

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly  
 405 410 415  
 His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys  
 420 425 430  
 Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg  
 435 440 445  
 Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr  
 450 455 460  
 Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser  
 465 470 475 480  
 Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln  
 485 490

&lt;210&gt; 6

&lt;211&gt; 813

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; Note =  
synthetic construct

&lt;221&gt; CDS

&lt;222&gt; (1)...(813)

&lt;400&gt; 6

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Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn	
1 5 10 15	

tcc aac atg gat gct gat tta tat ggg tat aaa tgg gct cgc gat aat	96
Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn	
20 25 30	

gtc ggg caa tca ggt gcg aca atc tat cga ttg tat ggg aag ccc gat	144
Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp	
35 40 45	

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gcg cca gag ttg ttt ctg aaa cat ggc aaa ggt agc gtt gcc aat gat	192
Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp	
50 55 60	

gtt aca gat gag atg gtc aga cta aac tgg ctg acg gaa ttt atg cct	240
Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro	
65 70 75 80	

ctt ccg acc atc aag cat ttt atc cgt act cct gat gat gca tgg tta	288
Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu	
85 90 95	

ctc acc act gcg atc ccc ggg aaa aca gca ttc cag gta tta gaa gaa	336
Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu	
100 105 110	

tat cct gat tca ggt gaa aat att gtt gat gcg ctg gca gtg ttc ctg	384
Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu	
115 120 125	
 cgc cggttgcatttcgttgcatttgtaattgtcctttaacagcgtat	432
Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp	
130 135 140	
 cgc gta ttt cgt ctc gct cag gcg caa tca cga atg aat aac ggt ttg	480
Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu	
145 150 155 160	
 gtt gat gcg agt gat ttt gat gac gag cgt aat ggc tgg cct gtt gaa	528
Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu	
165 170 175	
 caa gtc tgg aaa gaa atg cat aag ctt ttg cca ttc tca ccg gat tca	576
Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser	
180 185 190	
 gtc gtc act cat ggt gat ttc tca ctt gat aac ctt att ttt gac gag	624
Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu	
195 200 205	
 ggg aaa tta ata ggt tgt att gat gtt gga cga gtc gga atc gca gac	672
Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp	
210 215 220	
 cga tac cag gat ctt gcc atc cta tgg aac tgc ctc ggt gag ttt tct	720
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser	
225 230 235 240	
 cct tca tta cag aaa cgg ctt ttt caa aaa tat ggt att gat aat cct	768
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro	
245 250 255	
 gat atg aat aaa ttg cag ttt cat ttg atg ctc gat gag ttt ttc	813
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe	
260 265 270	

<210> 7  
<211> 271  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 7  
Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn  
1 5 10 15  
Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn  
20 25 30

Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp  
       35                        40                        45  
 Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp  
       50                        55                        60  
 Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro  
       65                        70                        75                        80  
 Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu  
       85                        90                        95  
 Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu  
       100                       105                       110  
 Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu  
       115                       120                       125  
 Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp  
       130                       135                       140  
 Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu  
       145                       150                       155                       160  
 Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu  
       165                       170                       175  
 Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser  
       180                       185                       190  
 Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu  
       195                       200                       205  
 Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp  
       210                       215                       220  
 Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser  
       225                       230                       235                       240  
 Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro  
       245                       250                       255  
 Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe  
       260                       265                       270

<210> 8  
<211> 5076  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

<400> 8	
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aggttagaagc caaggcggtc actgataatg accatgctaa tgccagagcg ttttcgcac	180
tggcttcaaa actgatcgaa acggagggtgg acccatccga cacgatccctt gacattggaa	240
gtgcggccgc cccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgtatgagat	300
gtgcggaaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgttaagg	360
aaataactga taagaattg gacaagaaaa tgaaggagct cgccggcgatc atgagcgacc	420
ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc	480
aagtgcgtt ttaccaggat gtatacgcgg ttgacggacc ctataactct ctacggctaa	540
cctgaatgga ctacgacata gtctagtcgg ccaagatgtt cccgttccag ccaatgtatc	600
cgatgcagcc aatgccctat cgcaaccgt tcggccggccc ggcgcaggccc tggttcccc	660
gaaccgaccc tttctggcg atgcagggtgc aggaattaac ccgctcgatg gctaaccctga	720
cgttcaagcca acgcgggac ggcgcacccgt agggggccatc cgctaagaaa cccaaagaagg	780
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agaaggctaa gacagggccg cctaattccga aggcacagaa tggaaacaag aagaagacca	900
acaagaaacc aggcagaga cagcgcatttgc tcatgaaatt ggaatctgac aagacgttcc	960

caatcatgtt	ggaagggaaag	ataaaacggct	acgcttgtgt	ggtcggaggg	aagttattca	1020
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aagcatccaa	atacgatctt	gagtatgcag	atgtgccaca	gaacatgcgg	gccgatacat	1140
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	gggaagagcg	cggccgcgcg	ctgggctacg	1800
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gcttatcatc	gataagctt	aatgcggtag	tttatcacag	ttaaattgct	aacgcagtca	4980
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<210> 9
<211> 1026
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

<221> CDS  
<222> (1) ... (1026)

<400> 9

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atg ttc ccg ttc cag cca atg tat ccg atg cag cca atg ccc tat cgc
Met Phe Pro Phe Gln Pro Met Tyr Pro Met Gln Pro Met Pro Tyr Arg
   1           5           10          15

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aac ccg ttc gcg gcc ccg cgc agg ccc tgg ttc ccc aga acc gac cct
Asn Pro Phe Ala Ala Pro Arg Arg Pro Trp Phe Pro Arg Thr Asp Pro
          20           25           30

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ttt ctg gcg atg cag gtg cag gaa tta acc cgc tcg atg gct aac ctg 144  
Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu  
35 40 45

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acg ttc aag caa cgc cg50 gac gc55 g cca cct gag gg60 g cca tcc gct aag
Thr Phe Lys Gln Arg Arg Asp Ala Pro Pro Glu Gly Pro Ser Ala Lys

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aaa ccg aag aag gag gcc tcg caa aaa cag aaa ggg gga ggc caa ggg 240  
Lys Pro Lys Lys Glu Ala Ser Gln Lys Gln Lys Gly Gly Gly Gln Gly  
65 70 75 80

aag aag aag aag aac caa ggg aag aag aag gct aag aca ggg ccg cct	288	
Lys Lys Lys Lys Asn Gln Gly Lys Lys Lys Ala Lys Thr Gly Pro Pro		
85	90	95

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ggc aag aga cag cgc atg gtc atg aaa ttg gaa tct gac aag acg ttc Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe 115 120 125	384
cca atc atg ttg gaa ggg aag ata aac ggc tac gct tgt gtg gtc gga Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly 130 135 140	432
ggg aag tta ttc agg ccg atg cat gtg gaa ggc aag atc gac aac gac Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp 145 150 155 160	480
gtt ctg gcc gcg ctt aag acg aag aaa gca tcc aaa tac gat ctt gag Val Leu Ala Ala Leu Lys Thr Lys Ala Ser Lys Tyr Asp Leu Glu 165 170 175	528
tat gca gat gtg cca cag aac atg cgg gcc gat aca ttc aaa tac acc Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr 180 185 190	576
cat gag aaa ccc caa ggc tat tac agc tgg cat cat gga gca gtc caa His Glu Lys Pro Gln Gly Tyr Ser Trp His His Gly Ala Val Gln 195 200 205	624
tat gaa aat ggg cgt ttc acg gtg ccg aaa gga gtt ggg gcc aag gga Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly 210 215 220	672
gac agc gga cga ccc att ctg gat aac cag gga cgg gtg gtc gct att Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile 225 230 235 240	720
gtg ctg gga ggt gtg aat gaa gga tct agg aca gcc ctt tca gtc gtc Val Leu Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val 245 250 255	768
atg tgg aac gag aag gga gtt acc gtg aag tat act ccg gag aac tgc Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys 260 265 270	816
gag caa tgg tca cta gtg acc acc atg tgt ctg ctc gcc aat gtg acg Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr 275 280 285	864
ttc cca tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu 290 295 300	912
act ttg gcc atg ctc agc gtt aac atc cct gct ggg agg atc agc cgt Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg 305 310 315 320	960

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aat tat tat aat tgg ctt ggt gct ggc tac tat tgt ggc cat gta cgt      1008
Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg
            325          330          335

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gct gac caa cca gaa aca 1026  
Ala Asp Gln Pro Glu Thr  
340

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<211> 342
<212> PRT
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

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Asn Pro Phe Ala Ala Pro Arg Arg Pro Trp Phe Pro Arg Thr Asp Pro
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Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu
   35         40         45

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Thr	Phe	Lys	Gln	Arg	Arg	Asp	Ala	Pro	Pro	Glu	Gly	Pro	Ser	Ala	Lys
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Lys	Pro	Lys	Lys	Glu	Ala	Ser	Gln	Lys	Gln	Lys	Gly	Gly	Gly	Gln	Gly
	65				70			75							80

Lys	Lys	Lys	Lys	Asn	Gln	Gly	Lys	Lys	Lys	Ala	Lys	Thr	Gly	Pro	Pro
				85				90					95		
Asn	Pro	Lys	Ala	Gln	Asn	Gly	Asn	Lys	Lys	Lys	Thr	Asn	Lys	Lys	Pro
			100					105					110		
Gly	Lys	Arg	Gln	Arg	Met	Val	Met	Lys	Leu	Glu	Ser	Asp	Lys	Thr	Phe
		115					120					125			
Pro	Ile	Met	Leu	Glu	Gly	Lys	Ile	Asn	Gly	Tyr	Ala	Cys	Val	Val	Gly
		130				135					140				

Gly	Lys	Leu	Phe	Arg	Pro	Met	His	Val	Glu	Gly	Lys	Ile	Asp	Asn	Asp
145					150					155					160
Val	Leu	Ala	Ala	Leu	Lys	Thr	Lys	Lys	Ala	Ser	Lys	Tyr	Asp	Leu	Glu
					165				170						175

Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr  
           180                 185                 190  
 His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln

195	200	205
Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly		
210	215	220
Asp Ser Gly Arg Pro Ile Leu Asp Asp Cys Gly Arg Val Val Ala Ile		

Asp	Ser	Gly	Arg	Phe	Ile	Leu	Asp	Asn	Gln	Gly	Arg	Val	Val	Ala	Ile
225															240
Val	Leu	Gly	Gly	Val	Asn	Glu	Gly	Ser	Arg	Thr	Ala	Leu	Ser	Val	Val

245	250	255
Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys		
260	265	270

Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr  
275 280 285

Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu  
 290 295 300  
 Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg  
 305 310 315 320  
 Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg  
 325 330 335  
 Ala Asp Gln Pro Glu Thr  
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<210> 11  
<211> 6989  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

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gtgcggaaaga tcggacaga ttgtataagt atgcaactaa gctgaagaaa aactgttaagg	360
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aagtgcgtgt ttaccaggat gtatacgcgg ttgacggacc ctataactct ctacggctaa	540
cctgaatggc ctacgacata gtctagccg ccaagatgtc actagtgacc accatgtgtc	600
tgctcgccaa tgtgacgttc ccatgtgtc aaccaccaat ttgctacgac agaaaaccag	660
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<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

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Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu  
20 25 30

gcc atg ctc agc gtt aac gtc aac ccg ggc tac gat gag ctg ctg  
Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu  
35 40 45

gaa gca gct gtt aag tgc ccc gga agg aaa agg aga tcc acc gag gag  
Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu  
50 55 60

ctg ttt aag gag tat aag cta acg cgc cct tac atg gcc aga tgc atc  
Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile  
65 70 75 80

aga tgt gca gtt ggg agc tgc cat agt cca ata gca atc gag gca gta Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val 85 90 95	288
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tat ggc ctg gat tcc tcc ggc aac tta aag ggc agg acc atg cgg tat Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr 115 120 125	384
gac atg cac ggg acc att aaa gag ata cca cta cat caa gtg tca ctc Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu 130 135 140	432
cat aca tct cgc ccg tgt cac att gtg gat ggg cac ggt tat ttc ctg His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu 145 150 155 160	480
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gat tcc gtc aca cac tcc tgc tcg gtg ccg tat gaa gtg aaa ttt aat Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn 180 185 190	576
cct gta ggc aga gaa ctc tat act cat ccc cca gaa cac gga gta gag Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu 195 200 205	624
caa gcg tgc caa gtc tac gca cat gat gca cag aac aga gga gct tat Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr 210 215 220	672
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ctg gca gac ggc aaa tgc acc gtg cct cta gca cca gaa cct atg ata Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile 325 330 335	1008
acc ttc ggt ttc aga tca gtg tca ctg aaa ctg cac cct aag aat ccc Thr Phe Gly Phe Arg Ser Val Ser Leu Lys Leu His Pro Lys Asn Pro 340 345 350	1056
aca tat cta acc acc cgc caa ctt gct gat gag cct cac tac acg cat Thr Tyr Leu Thr Arg Gln Leu Ala Asp Glu Pro His Tyr Thr His 355 360 365	1104
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att tgt gcc gcc att gca acc gtt tcc gtt gca gcg tct acc tgg ctg Ile Cys Ala Ala Ile Ala Thr Val Ser Val Ala Ala Ser Thr Trp Leu 435 440 445	1344
ttt tgc aga tct aga gtt gcg tgc cta act cct tac ccg cta aca cct Phe Cys Arg Ser Arg Val Ala Cys Leu Thr Pro Tyr Arg Leu Thr Pro 450 455 460	1392
aac gct agg ata cca ttt tgt ctg gct gtg ctt tgc tgc gcc cgc act Asn Ala Arg Ile Pro Phe Cys Leu Ala Val Leu Cys Cys Ala Arg Thr 465 470 475 480	1440
gcc cg <sup>g</sup> gcc gag acc acc tgg gag tcc ttg gat cac cta tgg aac aat Ala Arg Ala Glu Thr Thr Trp Glu Ser Leu Asp His Leu Trp Asn Asn 485 490 495	1488
aac caa cag atg ttc tgg att caa ttg ctg atc cct ctg gcc gcc ttg Asn Gln Gln Met Phe Trp Ile Gln Leu Leu Ile Pro Leu Ala Ala Leu 500 505 510	1536
atc gta gtg act cgc ctg ctc agg tgc gtg tgc tgt gtc gtg cct ttt Ile Val Val Thr Arg Leu Leu Arg Cys Val Cys Cys Val Val Pro Phe 515 520 525	1584

tta gtc atg gcc ggc gcc gca ggc gcc ggc gcc tac gag cac gcg acc Leu Val Met Ala Gly Ala Ala Gly Ala Gly Ala Tyr Glu His Ala Thr 530	535	540	1632	
acg atg ccg agc caa gcg gga atc tcg tat aac act ata gtc aac aga Thr Met Pro Ser Gln Ala Gly Ile Ser Tyr Asn Thr Ile Val Asn Arg 545	550	555	560	1680
gca ggc tac gca cca ctc cct atc agc ata aca cca aca aag atc aag Ala Gly Tyr Ala Pro Leu Pro Ile Ser Ile Thr Pro Thr Lys Ile Lys 565	570	575		1728
ctg ata cct aca gtg aac ttg gag tac gtc acc tgc cac tac aaa aca Leu Ile Pro Thr Val Asn Leu Glu Tyr Val Thr Cys His Tyr Lys Thr 580	585	590		1776
gga atg gat tca cca gcc atc aaa tgc tgc gga tct cag gaa tgc act Gly Met Asp Ser Pro Ala Ile Lys Cys Cys Gly Ser Gln Glu Cys Thr 595	600	605		1824
cca act tac agg cct gat gaa cag tgc aaa gtc ttc aca ggg gtt tac Pro Thr Tyr Arg Pro Asp Glu Gln Cys Lys Val Phe Thr Gly Val Tyr 610	615	620		1872
ccg ttc atg tgg ggt gca tat tgc ttt tgc gac act gag aac acc Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp Thr Glu Asn Thr 625	630	635	640	1920
caa gtc agc aag gcc tac gta atg aaa tct gac gac tgc ctt gcg gat Gln Val Ser Lys Ala Tyr Val Met Lys Ser Asp Asp Cys Leu Ala Asp 645	650	655		1968
cat gct gaa gca tat aaa gcg cac aca gcc tca gtg cag gcg ttc ctc His Ala Glu Ala Tyr Lys Ala His Thr Ala Ser Val Gln Ala Phe Leu 660	665	670		2016
aac atc aca gtg gga gaa cac tct att gtg act acc gtg tat gtg aat Asn Ile Thr Val Gly Glu His Ser Ile Val Thr Thr Val Tyr Val Asn 675	680	685		2064
gga gaa act cct gtg aat ttc aat ggg gtc aaa tta act gca ggt ccg Gly Glu Thr Pro Val Asn Phe Asn Gly Val Lys Leu Thr Ala Gly Pro 690	695	700		2112
ctt tcc aca gct tgg aca ccc ttt gat cgc aaa atc gtg cag tat gcc Leu Ser Thr Ala Trp Thr Pro Phe Asp Arg Lys Ile Val Gln Tyr Ala 705	710	715	720	2160
ggg gag atc tat aat tat gat ttt cct gag tat ggg gca gga caa cca Gly Glu Ile Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Gly Gln Pro 725	730	735		2208
gga gca ttt gga gat ata caa tcc aga aca gtc tca agc tca gat ctg Gly Ala Phe Gly Asp Ile Gln Ser Arg Thr Val Ser Ser Ser Asp Leu 740	745	750		2256

tat gcc aat acc aac cta gtg ctg cag aga ccc aaa gca gga gcg atc 2304  
 Tyr Ala Asn Thr Asn Leu Val Leu Gln Arg Pro Lys Ala Gly Ala Ile  
 755 760 765

cac gtg cca tac act cag gca cct tcg ggt ttt gag caa tgg aag aaa 2352  
 His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys  
 770 775 780

gat aaa gct cca tca ttg aaa ttt acc gcc cct ttc gga tgc gaa ata 2400  
 Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile  
 785 790 795 800

tat aca aac ccc att cgc gcc gaa aac tgt act gta ggg tca att cca 2448  
 Tyr Thr Asn Pro Ile Arg Ala Glu Asn Cys Thr Val Gly Ser Ile Pro  
 805 810 815

tta gcc ttt gac att ccc gac gcc ttg ttc acc agg gtg tca gaa aca 2496  
 Leu Ala Phe Asp Ile Pro Asp Ala Leu Phe Thr Arg Val Ser Glu Thr  
 820 825 830

ccg aca ctt tca gcg gcc gaa tgc act ctt aac gag tgc gtg tat tct 2544  
 Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser  
 835 840 845

tcc gac ttt ggt ggg atc gcc acg gtc aag tac tcg gcc agc aag tca 2592  
 Ser Asp Phe Gly Ile Ala Thr Val Lys Tyr Ser Ala Ser Lys Ser  
 850 855 860

ggc aag tgc gca gtc cat gtg cca tca ggg act gct acc cta aaa gaa 2640  
 Gly Lys Cys Ala Val His Val Pro Ser Gly Thr Ala Thr Leu Lys Glu  
 865 870 875 880

gca gca gtc gag cta acc gag caa ggg tcg gcg act atc cat ttc tcg 2688  
 Ala Ala Val Glu Leu Thr Glu Gln Gly Ser Ala Thr Ile His Phe Ser  
 885 890 895

acc gca aat atc cac ccg gag ttc agg ctc caa ata tgc aca tca tat 2736  
 Thr Ala Asn Ile His Pro Glu Phe Arg Leu Gln Ile Cys Thr Ser Tyr  
 900 905 910

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gtt acg tgc aaa ggt gat tgt cac ccc ccg aaa gac cat att gtg aca 2784  
 Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr  
 915 920 925

cac cct cag tat cac gcc caa aca ttt aca gcc gcg gtg tca aaa acc 2832  
 His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr  
 930 935 940

gcg tgg acg tgg tta aca tcc ctg ctg gga gga tca gcc gta att att 2880  
 Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile  
 945 950 955 960

ata att ggc ttg gtg ctg gct act att gtg gcc atg tac gtg ctg acc 2928  
 Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr  
 965 970 975

aac cag aaa cat aat  
 Asn Gln Lys His Asn  
 980

2943

<210> 13  
 <211> 981  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

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 Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu  
 20 25 30  
 Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu  
 35 40 45  
 Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu  
 50 55 60  
 Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile  
 65 70 75 80  
 Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val  
 85 90 95  
 Lys Ser Asp Gly His Asp Gly Tyr Val Arg Leu Gln Thr Ser Ser Gln  
 100 105 110  
 Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr  
 115 120 125  
 Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu  
 130 135 140  
 His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu  
 145 150 155 160  
 Leu Ala Arg Cys Pro Ala Gly Asp Ser Ile Thr Met Glu Phe Lys Lys  
 165 170 175  
 Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn  
 180 185 190  
 Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu  
 195 200 205  
 Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr  
 210 215 220  
 Val Glu Met His Leu Pro Gly Ser Glu Val Asp Ser Ser Leu Val Ser  
 225 230 235 240  
 Leu Ser Gly Ser Ser Val Thr Val Thr Pro Pro Val Gly Thr Ser Ala  
 245 250 255  
 Leu Val Glu Cys Glu Cys Gly Gly Thr Lys Ile Ser Lys Thr Ile Asn  
 260 265 270  
 Lys Thr Lys Gln Phe Ser Gln Cys Thr Lys Lys Glu Gln Cys Arg Ala  
 275 280 285  
 Tyr Arg Leu Gln Asn Asp Lys Trp Val Tyr Asn Ser Asp Lys Leu Pro  
 290 295 300  
 Lys Ala Ala Gly Ala Thr Leu Lys Gly Lys Leu His Val Pro Phe Leu  
 305 310 315 320

Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile  
                  325                 330                 335  
 Thr Phe Gly Phe Arg Ser Val Ser Leu Lys Leu His Pro Lys Asn Pro  
                  340                 345                 350  
 Thr Tyr Leu Thr Thr Arg Gln Leu Ala Asp Glu Pro His Tyr Thr His  
                  355                 360                 365  
 Glu Leu Ile Ser Glu Pro Ala Val Arg Asn Phe Thr Val Thr Gly Lys  
                  370                 375                 380  
 Gly Trp Glu Phe Val Trp Gly Asn His Pro Pro Lys Arg Phe Trp Ala  
                  385                 390                 395                 400  
 Gln Glu Thr Ala Pro Gly Asn Pro His Gly Leu Pro His Glu Val Ile  
                  405                 410                 415  
 Thr His Tyr Tyr His Arg Tyr Pro Met Ser Thr Ile Leu Gly Leu Ser  
                  420                 425                 430  
 Ile Cys Ala Ala Ile Ala Thr Val Ser Val Ala Ala Ser Thr Trp Leu  
                  435                 440                 445  
 Phe Cys Arg Ser Arg Val Ala Cys Leu Thr Pro Tyr Arg Leu Thr Pro  
                  450                 455                 460  
 Asn Ala Arg Ile Pro Phe Cys Leu Ala Val Leu Cys Cys Ala Arg Thr  
                  465                 470                 475                 480

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Ala Arg Ala Glu Thr Thr Trp Glu Ser Leu Asp His Leu Trp Asn Asn  
                  485                 490                 495  
 Asn Gln Gln Met Phe Trp Ile Gln Leu Leu Ile Pro Leu Ala Ala Leu  
                  500                 505                 510  
 Ile Val Val Thr Arg Leu Leu Arg Cys Val Cys Cys Val Val Pro Phe  
                  515                 520                 525  
 Leu Val Met Ala Gly Ala Ala Gly Ala Gly Ala Tyr Glu His Ala Thr  
                  530                 535                 540  
 Thr Met Pro Ser Gln Ala Gly Ile Ser Tyr Asn Thr Ile Val Asn Arg  
                  545                 550                 555                 560  
 Ala Gly Tyr Ala Pro Leu Pro Ile Ser Ile Thr Pro Thr Lys Ile Lys  
                  565                 570                 575  
 Leu Ile Pro Thr Val Asn Leu Glu Tyr Val Thr Cys His Tyr Lys Thr  
                  580                 585                 590  
 Gly Met Asp Ser Pro Ala Ile Lys Cys Cys Gly Ser Gln Glu Cys Thr  
                  595                 600                 605  
 Pro Thr Tyr Arg Pro Asp Glu Gln Cys Lys Val Phe Thr Gly Val Tyr  
                  610                 615                 620

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Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp Thr Glu Asn Thr  
                  625                 630                 635                 640  
 Gln Val Ser Lys Ala Tyr Val Met Lys Ser Asp Asp Cys Leu Ala Asp  
                  645                 650                 655  
 His Ala Glu Ala Tyr Lys Ala His Thr Ala Ser Val Gln Ala Phe Leu  
                  660                 665                 670  
 Asn Ile Thr Val Gly Glu His Ser Ile Val Thr Thr Val Tyr Val Asn  
                  675                 680                 685  
 Gly Glu Thr Pro Val Asn Phe Asn Gly Val Lys Leu Thr Ala Gly Pro  
                  690                 695                 700  
 Leu Ser Thr Ala Trp Thr Pro Phe Asp Arg Lys Ile Val Gln Tyr Ala  
                  705                 710                 715                 720  
 Gly Glu Ile Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Gly Gln Pro  
                  725                 730                 735  
 Gly Ala Phe Gly Asp Ile Gln Ser Arg Thr Val Ser Ser Ser Asp Leu  
                  740                 745                 750  
 Tyr Ala Asn Thr Asn Leu Val Leu Gln Arg Pro Lys Ala Gly Ala Ile  
                  755                 760                 765

His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys  
 770 775 780  
 Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile  
 785 790 795 800  
 Tyr Thr Asn Pro Ile Arg Ala Glu Asn Cys Thr Val Gly Ser Ile Pro  
 805 810 815  
 Leu Ala Phe Asp Ile Pro Asp Ala Leu Phe Thr Arg Val Ser Glu Thr  
 820 825 830  
 Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser  
 835 840 845  
 Ser Asp Phe Gly Gly Ile Ala Thr Val Lys Tyr Ser Ala Ser Lys Ser  
 850 855 860  
 Gly Lys Cys Ala Val His Val Pro Ser Gly Thr Ala Thr Leu Lys Glu  
 865 870 875 880  
 Ala Ala Val Glu Leu Thr Glu Gln Gly Ser Ala Thr Ile His Phe Ser  
 885 890 895  
 Thr Ala Asn Ile His Pro Glu Phe Arg Leu Gln Ile Cys Thr Ser Tyr  
 900 905 910

Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr  
 915 920 925  
 His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr  
 930 935 940  
 Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile  
 945 950 955 960  
 Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr  
 965 970 975  
 Asn Gln Lys His Asn  
 980

<210> 14  
 <211> 12379  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence; Note =  
 synthetic construct

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 aggttagaagc caagcaggc actgataatg accatgctaa tgccagagcg ttttcgcac 180  
 tggcttcaaactgtatcgaa acggagggtgg acccatccga cacgatcctt gacattggaa 240  
 gtgcggccgc ccgcagaatgt tattctaagc acaagtatca ttgtatctgt ccgatgagat 300  
 gtgcggaa tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaaagg 360  
 aaataactga taaggaattt gacaagaaaa tgaaggagct cgccggcgatc atgagcgacc 420  
 ctgaccttggaa aacttgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc 480  
 aagtgcgtgtt accaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag 540  
 ccaataaggg agttagatgc gcctacttggaa taggctttga caccacccct tttatgttta 600  
 agaacttggc tggagcatat ccatcataact ctaccaactg ggccgacgaa accgtgtttaa 660  
 cggctcgtaa cataggccta tgcagctctg acgttatggaa gcggtcacgt agagggatgt 720  
 ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctt gttggctcga 780  
 ccatctacca cgagaagagg gacttactga ggagctggca cctgcgtct gtatttcact 840  
 tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg 900  
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 ccatgcacccg cgagggttcc ttgtgtcgca aagtgcacaga cacattcaac ggggagaggg 1020

tctctttcc cgtgtgcacg tatgtgccag ctacattgtg tgaccaaatg actggcatac	1080
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atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa	1440
caagaatcag gaaaatgtt gaggagaca aggagccgtc accttcatt accggcgagg	1500
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 Lys Ala Leu Thr Ala Ile Cys Glu Glu Met Glu Lys Glu Gly Lys Ile  
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aca aaa att ggg cct gaa aat cca tat aac act cca ata ttc gcc ata 192  
 Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile  
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115 120 125	
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275 280 285	
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## **synthetic construct**

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 Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr  
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 Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg  
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Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile  
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 Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Ala Lys Asn  
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 Pro Glu Ile Val Ile Tyr Gln His Met Ala Ala Leu Tyr Val Gly Ser  
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 Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Glu  
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 His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys  
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 Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Thr Ser Gln Ile Tyr  
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 Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys  
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 Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr  
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synthetic construct

DRAFT - NOT FOR FILING

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Leu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu
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cca att cct ata cat tat tgt gct cca gct ggt tat gcg att cta aag Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys 210 215 220	672
tgt aat aat aag aca ttc aat ggg aca gga cca tgc aat aat gtc agc Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser 225 230 235 240	720
aca gta caa tgt aca cat gga att atg cca gtg gta tca actcaa tta Thr Val Gln Cys Thr His Gly Ile Met Pro Val Val Ser Thr Gln Leu 245 250 255	768
ctg tta aat ggt agc cta gca gaa gaa gag ata ata att aga tct gaa Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Arg Ser Glu 260 265 270	816
aat ctg aca aac aat atc aaa aca ata ata gtc cac ctt aat aaa tct Asn Leu Thr Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser 275 280 285	864
gta gaa att gtg tgt aca aga ccc aac aat aat aca aga aaa agt ata Val Glu Ile Val Cys Thr Arg Pro Asn Asn Thr Arg Lys Ser Ile 290 295 300	912
agg ata gga cca gga caa aca ttc tat gca aca ggt gaa ata ata gga Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly 305 310 315 320	960
aac ata aga gaa gca cat tgt aac att agt aaa agt aac tgg acc agt Asn Ile Arg Glu Ala His Cys Asn Ile Ser Lys Ser Asn Trp Thr Ser 325 330 335	1008
act tta gaa cag gta aag aaa aaa tta aaa gaa cac tac aat aag aca Thr Leu Glu Gln Val Lys Lys Lys Leu Lys Glu His Tyr Asn Lys Thr 340 345 350	1056
ata gaa ttt aac cca ccc tca gga ggg gat cta gaa gtt aca aca cat Ile Glu Phe Asn Pro Pro Ser Gly Gly Asp Leu Glu Val Thr Thr His 355 360 365	1104
agc ttt aat tgt aga gga gaa ttt ttc tat tgc aat aca aca aaa ctg Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu 370 375 380	1152
ttt tca aac aac agt gat tca aac aac gaa acc atc aca ctc cca tgc Phe Ser Asn Asn Ser Asp Ser Asn Asn Glu Thr Ile Thr Leu Pro Cys 385 390 395 400	1200

aag ata aaa caa att ata aac atg tgg cag aag gta gga cga gca atg 1248  
 Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Arg Ala Met  
 405 410 415

tat gcc cct ccc att gaa gga aac ata aca tgt aaa tca aat atc aca 1296  
 Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr  
 420 425 430

gga cta cta ttg aca cgt gat gga gga aag aat aca aca aat gag ata 1344  
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile  
 435 440 445

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ttc aga ccg gga gga gga aat atg aag gac aat tgg aga agt gaa tta 1392  
 Phe Arg Pro Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu  
 450 455 460

tat aaa tat aaa gtg gta gaa att gag cca ttg gga gta gca ccc act 1440  
 Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr  
 465 470 475 480

aaa tca aaa agg aga gtg gtg gag aga gaa aaa aga gca gtg gga cta 1488  
 Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu  
 485 490 495

gga gct gta ctc ctt ggg ttc ttg gga gca gca gga agc act atg ggc 1536  
 Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly  
 500 505 510

gcg gcg tca ata acg ctg acg gta cag gcc aga caa ctg ttg tct ggt 1584  
 Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly  
 515 520 525

ata gtg caa cag caa agc aat ttg ctg aga gct ata gag gcg caa cag 1632  
 Ile Val Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln  
 530 535 540

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cat atg ttg caa ctc acg gtc tgg ggc att aag cag ctc cag aca aga 1680  
 His-Met-Leu-Gln-Leu-Thr-Val-Trp-Gly-Ile-Lys-Gln-Leu-Gln-Thr-Arg  
 545 550 555 560

gtc ttg gct ata gag aga tac cta aag gat caa cag ctc cta ggg ctt 1728  
 Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu  
 565 570 575

tgg ggc tgc tct gga aaa atc atc tgc acc act gct gtg cct tgg aac 1776  
 Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn  
 580 585 590

tcc agt tgg agt aat aaa tct caa gaa gat att tgg gat aac atg acc 1824  
 Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr  
 595 600 605

tgg atg cag tgg gat aga gaa att agt aat tac aca ggc aca ata tat 1872  
 Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr  
 610 615 620

agg tta ctt gaa gac tcg caa aac cag cag gag aaa aat gaa aaa gat Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp 625 630 635 640	1920
tta tta gca ttg gac agt tgg aaa aac ttg tgg aat tgg ttt aac ata Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile 645 650 655	1968
aca aat tgg ctg tgg tat ata aaa ata ttc atc atg ata gta gga ggc Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly 660 665 670	2016
ttg ata ggt ttg aga ata att ttt ggt gta ctc gct ata gtg aaa aga Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg 675 680 685	2064
gtt agg cag gga tac tca cct ttg tcg ttt cag acc ctt acc cca agc Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser 690 695 700	2112
ccg agg ggt ccc gac agg ctc gga aga atc gaa gaa ggt gga gag Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Gly Gly Glu 705 710 715 720	2160
caa gac aaa gac aga tcc att cga tta gtg agc gga ttc tta gca ctt Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu 725 730 735	2208
gcc tgg gac gat ctg cgg agc ctg tgc ctc ttc agc tac cac cac ttg Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu 740 745 750	2256
aga gac ttc ata ttg att gca gcg aga gca gcg gaa ctt ctg gga cgc Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg 755 760 765	2304
agc agt ctc agg gga ctg cag aga ggg tgg gaa gcc ctt aag tat ctg Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu 770 775 780	2352
gga aat ctt gtg cag tat ggg ggt ctg gag cta aaa aga agt gct att Gly Asn Leu Val Gln Tyr Gly Leu Glu Leu Lys Arg Ser Ala Ile 785 790 795 800	2400
aaa ctg ttt gat acc ata gca ata gca gta gct gaa gga aca gat agg Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg 805 810 815	2448
att ctt gaa gta ata cag aga att tgt aga gct atc cgc cac ata cct Ile Leu Glu Val Ile Gln Arg Ile Cys Arg Ala Ile Arg His Ile Pro 820 825 830	2496
ata aga ata aga cag ggc ttt gaa gca gct ttg caa Ile Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln 835 840	2532

<211> 844  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; Note =  
synthetic construct

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Gly Thr Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Val Gly Asn  
20 25 30  
Leu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu  
35 40 45  
Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys  
50 55 60  
Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro  
65 70 75 80  
Asn Pro Arg Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met  
85 90 95  
Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu  
100 105 110  
Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val  
115 120 125  
Thr Leu Asn Cys Thr Asn Ala Pro Ala Tyr Asn Asn Ser Met His Gly  
130 135 140  
Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Glu Ile Arg Asp Arg  
145 150 155 160  
Lys Gln Lys Ala Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu  
165 170 175  
Asn Arg Arg Glu Asn Asn Gly Thr Gly Glu Tyr Ile Leu Ile Asn  
180 185 190  
Cys Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Thr Phe Asp  
195 200 205  
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys  
210 215 220  
Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser  
225 230 235 240  
Thr Val Gln Cys Thr His Gly Ile Met Pro Val Val Ser Thr Gln Leu  
245 250 255  
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Arg Ser Glu  
260 265 270  
Asn Leu Thr Asn Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser  
275 280 285  
Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile  
290 295 300  
  
Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly  
305 310 315 320  
Asn Ile Arg Glu Ala His Cys Asn Ile Ser Lys Ser Asn Trp Thr Ser  
325 330 335  
Thr Leu Glu Gln Val Lys Lys Leu Lys Glu His Tyr Asn Lys Thr  
340 345 350  
Ile Glu Phe Asn Pro Pro Ser Gly Gly Asp Leu Glu Val Thr Thr His  
355 360 365

Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu  
 370 375 380  
 Phe Ser Asn Asn Ser Asp Ser Asn Asn Glu Thr Ile Thr Leu Pro Cys  
 385 390 395 400  
 Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Arg Ala Met  
 405 410 415  
 Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr  
 420 425 430  
 Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile  
 435 440 445  
 Phe Arg Pro Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu  
 450 455 460  
 Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr  
 465 470 475 480  
 Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu  
 485 490 495  
 Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly  
 500 505 510  
 Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly  
 515 520 525  
 Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln  
 530 535 540  
 His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg  
 545 550 555 560  
 Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu  
 565 570 575  
 Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn  
 580 585 590  
 Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr  
 595 600 605  
 Trp Met Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr  
 610 615 620  
 Arg Leu Leu Glu Asp Ser Gln Asn Gln Glu Lys Asn Glu Lys Asp  
 625 630 635 640  
 Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile  
 645 650 655  
 Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly  
 660 665 670  
 Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg  
 675 680 685  
 Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser  
 690 695 700  
 Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Glu  
 705 710 715 720  
 Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu  
 725 730 735  
  
 Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu  
 740 745 750  
 Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg  
 755 760 765  
 Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu  
 770 775 780  
 Gly Asn Leu Val Gln Tyr Gly Gly Leu Glu Leu Lys Arg Ser Ala Ile  
 785 790 795 800  
 Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg  
 805 810 815

Ile Leu Glu Val Ile Gln Arg Ile Cys Arg Ala Ile Arg His Ile Pro  
820 825 830  
Ile Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln  
835 840

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